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1 **Genetic parameters of Visual Image Analysis primal cut carcass traits of**
2 **commercial prime beef slaughter animals**

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9
10 Short title: Genetic parameters of beef primal cuts

11
12 **Abstract**

13 Visual image Analysis (VIA) of carcass traits provides the opportunity to estimate
14 carcass primal cut yields on large numbers of slaughter animals. This allows
15 carcasses to be better differentiated and farmers to be paid based on the primal cut
16 yields. It also creates more accurate genetic selection due to high volumes of data
17 which enables breeders to breed cattle that better meet the abattoir specifications
18 and market requirements. In order to implement genetic evaluations for VIA primal
19 cut yields, genetic parameters must first be estimated and that was the aim of this
20 study. Slaughter records from the UK prime slaughter population for VIA carcass
21 traits was available from two processing plants. After edits, there were 17,765 VIA
22 carcass records for six primal cut traits, carcass weight as well as the EUROP
23 conformation and fat class grades. Heritability estimates after traits were adjusted for
24 age ranged from 0.32 (0.03) for EUROP fat to 0.46 (0.03) for VIA Topside primal cut
25 yield. Adjusting the VIA primal cut yields for carcass weight reduced the heritability
26 estimates, with estimates of primal cut yields ranging from 0.23 (0.03) for Fillet to

27 0.29 (0.03) for Knuckle. Genetic correlations between VIA primal cut yields adjusted
28 for carcass weight were very strong, ranging from 0.40 (0.06) between Fillet and
29 Striploin to 0.92 (0.02) between Topside and Silverside. EUROP conformation was
30 also positively correlated with the VIA primal cuts with genetic correlation estimates
31 ranging from 0.59 to 0.84, while EUROP fat was estimated to have moderate
32 negative correlations with primal cut yields, estimates ranged from -0.11 to -0.46.
33 Based on these genetic parameter estimates, genetic evaluation of VIA primal cut
34 yields can be undertaken to allow the UK beef industry to select carcasses that better
35 meet abattoir specification and market requirements.

36

37 **Keywords:** Visual image Analysis (VIA), genetic parameter estimation, prime
38 slaughter beef cattle, carcass traits

39

40 **Implications**

41 Visual image Analysis primal cut yields are moderately heritable with sufficient
42 genetic variability to allow response to selection. Primal cut yields were estimated to
43 have strong, but not unity, genetic correlations and breeders will be able to
44 genetically select animals that produce carcasses with a greater proportion of the
45 weight in the more valuable primal cuts. This will improve genetic progress for
46 abattoir carcass traits as the EBVs will be based on actual abattoir carcass data,
47 rather than proxy traits as in the pedigree sector. As carcass traits are end of life
48 traits these genetic parameters will also enable genomic selection to be implemented
49 to increase genetic progress estimated early in life.

50

51 **Introduction**

52 Genetic improvement in the UK beef industry has traditionally been implemented in
53 the purebred pedigree sector through voluntary performance recording. Selection for
54 carcass traits has been via Estimated Breeding Values (EBVs) produced from
55 recording proxy traits. Live weight at 400 days of age is a proxy for carcass weight
56 and ultrasound scans for muscle and fat depth are proxies for carcass conformation
57 and fat. However due to the cost of ultrasound scanning, only a relatively small
58 proportion of the purebred population have these carcass traits recorded (Moore *et*
59 *al.*, 2014). Whilst genetic improvement is made in the commercial sector through the
60 purchase of superior purebred bulls, the market signals to pedigree breeders are
61 diluted since commercial farmers are paid based for the carcass on the EUROP
62 classification system.

63

64 In the European Union, beef carcasses are assessed using the EUROP classification
65 system (European Council regulations 1208/81 and 2930/81). Carcasses are valued
66 per kg carcass weight at the base rate price (varies depending on breed, age and the
67 animals type; steer, heifer, cow etc.) with a penalty or premium added based the
68 EUROP conformation and fat class of the carcass. EUROP classification uses letters
69 E (excellent), to P (poor) to grade conformation with particular emphasis on the
70 round, back and shoulder. A five point numeric scale is used to classify the amount of
71 subcutaneous fat on the carcass and in the thoracic cavity, where the number one
72 represents none or low fat cover and number five represents very high fat. Often the
73 EUROP fat scale of five points is subdivided into three subclasses (-, = or +)
74 (MLCSL, 2014).

75

76 Advances in imaging technologies such as Visual Image Analysis (VIA) provide the
77 opportunity to mechanically grade carcasses, at line speed, for the EUROP traits but
78 in addition for individual primal cut yields. This creates the underlying framework to
79 undertake genetic evaluation for these traits using large volumes of commercial
80 abattoir data. In Ireland, VIA carcass traits have been investigated (Pabiou *et al.*,
81 2009; 2011a; 2011b; 2012) and found to have moderate to high heritabilities with
82 strong, but not unity, positive genetic correlations between the VIA primal cuts. In
83 these studies, carcass weight and EUROP traits conformation and fat were also
84 considered and found to have moderate heritability. Carcass weight and EUROP
85 conformation was estimated to have moderate to strong positive genetic correlations
86 with the individual VIA primal cuts, whilst EUROP fat had moderately negative
87 genetic correlations with the individual VIA primal cuts. Given the strong genetic
88 correlations between the VIA primal cuts, Pabiou *et al.* (2011a; 2011b) combined the
89 individual primal cuts into three categories based on the value of the primal cut (high,
90 medium, low). Again moderate to high heritabilities were estimated.

91
92 The objective of this study was to use VIA carcass information from the cross bred
93 UK commercial prime slaughter population to estimate genetic parameters for
94 individual primal cut yields, carcass weight and EUROP conformation and fat class to
95 enable subsequent genetic evaluation of carcass traits.

96

97 **Material and methods**

98 *Data Sources*

99 Carcass data (carcass measurements, animal identification, dates of birth and death,
100 animal breed and type of slaughter animal (i.e. steer or young bull)) was collected

101 from two abattoirs fitted with VBS2000 VIA machines (E+V Technology,
102 <http://www.eplusv.de/>), installed to grade carcasses at slaughter. One side of the
103 carcass was positioned on a holding frame while a 2D and 3D image was taken by
104 the VIA machine's mounted digital camera using previously calibrated lighting
105 arrangements. The resulting images are analysed using E+V software and prediction
106 equations to predict six individual primal cuts from the hindquarter; Topside,
107 Silverside, Striploin, Fillet, Knuckle and Rump, as well as carcass weight and the
108 EUROP classification for conformation and fat. The predicted VIA primal cut yields
109 were then multiplied by 2 to represent both sides of the carcass. Carcass weight and
110 all six primal cut yields were estimated in kg, while EUROP conformation and fat was
111 recorded according to EUROP standards and then recoded to a 15 point numerical
112 scale described by Hickey *et al.* (2007). To increase the scale of variation the
113 converted conformation and fat measurements was multiplied by three making the
114 range 1-45.

115

116 Pedigree and additional animal information was obtained from the British Cattle
117 Movement Service (BCMS) database, where it has been compulsory to register all
118 dairy and beef cattle in the UK since 1996. For every animal, the BCMS database
119 records the dam, date of birth, details of each farm movement by the animal, breed,
120 sex and dates of death. In addition the sire can be recorded, but is not compulsory,
121 and is recorded in approximately a third of registered animals. Additional pedigree
122 information was also available from the UK dairy milk recording organizations in the
123 UK as well as the pedigree herd books for a number of different dairy and beef
124 breeds. All sources of pedigree are combined to form a single UK dairy and beef
125 'super pedigree' that contains all known animals in the UK as well as all known

126 pedigree, i.e. if sire is recorded in one data source and dam in another source, the
127 super pedigree is the only pedigree that contains both the sire and the dam.

128

129 *Calculation of proportion of each breed*

130 The animals' breed is supplied in several sources of data. This is usually just a single
131 breed code and does not enable the precise breed make up to be captured,
132 especially of cross breeds, and thus allow breed and hybrid vigour effects to be
133 accounted for. Therefore, for all animals in the super pedigree the proportion of each
134 breed (PEB) is calculated. The PEB of each animal is simply half the PEB of the sire
135 plus half the PEB of the dam. For example, an animal with a sire that is 100%
136 Limousin and a dam that is 50% Holstein Friesian : 50% Limousin will end up with a
137 PEB of 75% Limousin : 25% Holstein Friesian. This approach is iterative, with
138 parents first needing PEB calculated before progeny PEB can be computed. Where
139 one or both parents are unknown a set of assumptions are applied to obtain an
140 estimate of the PEB. When both parents are unknown and if the animal is included in
141 the BASCO database (database storing pedigree and performance recording
142 information for some beef breeds in the UK) with breed make up recorded, then the
143 PEB is set to match the breed make up from BASCO. If the animal is not recorded in
144 BASCO, then it is assumed to be 100% of the breed code supplied in BCMS data. In
145 cases where one parent is known and the other is unknown, the same assumptions
146 as above apply but with the PEB adjusted for the contribution of the known parent.
147 For example, if the breed code in the BCMS data is Limousin, the sire is unknown
148 and the dam is 100% Holstein Frisian then the PEB for the animal would be 50%
149 Limousin : 50% Holstein Frisian.

150

151 *Heterosis and recombination coefficients*

152 To enable the effects of hybrid vigour to be considered in the analysis, heterosis and
153 recombination effects were calculated for a limited number of breed 'type' categories.
154 With such a large number of breeds represented in the data, it was not practical to
155 model heterosis effects for every combination, therefore breeds were grouped into
156 four breed types; dairy, native UK beef breeds, continental beef breeds and
157 remaining breeds (of which there were few). The PEB was then concatenated into
158 these breed types such that a 50% Limousin : 50% Charolais would be 100%
159 continental. For each animal and each combination of breed type (six) heterosis and
160 recombination coefficients were computed where A and B represent the proportion of
161 genes from the two breed types considered and s and d denote sire and dam,
162 respectively (Van der Werf and De Boer, 1989).

163

164 Heterozygosis $_{AB} = A_d \cdot B_s + A_s \cdot B_d$

165 Recombination loss $_{AB} = A_s \cdot B_s + A_d \cdot B_d$

166

167 *Dataset edits*

168 A total of 111,394 prime slaughter commercial carcasses records were available from
169 two abattoir sites. Animals were defined as being prime slaughter if the abattoir
170 classification was one of three categories: heifer (H), steer (S) and young bull (YB).
171 All animals were slaughtered between 2012 and 2014 – although one site only had
172 kill data for a portion of 2014. Records were removed if: the sire was unknown
173 (n=74,844); the age at slaughter was less than 365 days (12 months) (n=13) or
174 greater than 1095 days (36 months) for heifers and steers (n=1,698) and greater than
175 730 (24 months) for young bulls (n=44); the animal was an outlier (defined by \pm three

176 standard deviations from the mean within sire breed and category (H;S;YB)) for any
177 of the VIA primal cut yields, carcass weight or EUROP conformation and fat traits
178 (n=886); the sire was not purebred (purebred defined as being 87.5+% of one breed)
179 (n=670); the breed of the sire was from a numerically small breed (defined as breeds
180 with less than 200 animals in the dataset) (n=668); the animal belonged to a paternal
181 half sib family with less than three half sibs (n=4,955); the animal came from a birth
182 herd with less than three records (n=465); the animal was in a finishing herd with less
183 than three records (n=665); there were fewer than three animals in the birth season –
184 herd contemporary group, where season was defined in four month blocks (n=3,314);
185 the animal was in a single sire contemporary group (n=5,296). After the above edits,
186 only 111 records remained from the new VIA abattoir site, so these were removed
187 leaving only one site in the analysis.

188

189 *Final dataset*

190 After edits, 17,765 records remained from one abattoir, covering 11 different sire
191 breeds from 660 birth herds and 668 finishing herds. Of these records there were
192 4,758 heifers, 7,642 steers and 5,365 young bulls. Animals were born between
193 February 2010 and August 2013 and slaughtered between July 2012 and September
194 2014. The population consisted of 1,379 (7.8%) purebred animals and 16,386
195 (92.2%) crossbred animals. Based on the sire breed, the more numerous breeds
196 were Charolais (25.2%), Limousin (18.8%), Simmental (18.6%), Angus (17.7%) and
197 Holstein Frisian (10.7%). The remaining seven breeds combined accounted for 9.3%
198 of the edited dataset. A three generation pedigree (n=87,788) was extracted from the
199 bovine super pedigree for all animals remaining in the edited dataset.

200

201 *Statistical analysis*

202 The statistical model was developed using the PROC MIXED procedure in the SAS
203 software (SAS Institute, 2007). Fixed effects were determined from a sire model
204 using backwards elimination to remove terms that were not significant. Significance
205 was determined using the F test and $P < 0.05$. First order interactions were also fitted.
206 The factors considered as fixed class effects were abattoir sex category (H, S or YB),
207 birth season herd contemporary groups (BSH), finishing herd and kill season (defined
208 as four month periods, starting from February). Considered as co-variate effects were
209 age at slaughter (linear and quadratic), dam age in days (linear and quadratic), the
210 percentage of dairy breeds in the dam, and the heterosis and recombination
211 coefficients for each breed type combination (described above).

212

213 For all traits abattoir sex category, BSH, finishing herd, kill season, slaughter age
214 (linear and quadratic), linear dam age and percentage of dairy breeds in the dam
215 were significant. Heterosis effects between the dairy, native beef and continental
216 beef breed types were significant, but not those crosses involving the remaining
217 breed types, most likely due to the small number of animals in the UK that cannot be
218 grouped into the three main breed types. Recombination effects were significant for
219 dairy * native beef breed type crosses, and for most of the traits the native beef *
220 remaining breed type crosses. Significant first order interactions were abattoir sex
221 category with the following terms; kill season, age at slaughter and percentage of
222 dairy in the dam. In addition, interactions with age at slaughter with percentage of
223 dairy in the dam and dam age and the interaction between dam age and the
224 percentage of dairy in the dam were significant.

225

226 Uni-variate co-variance components were estimated using single trait animal models
227 (ASReml; Gilmour *et al.*, 2009). Relationships amongst animals were accounted for
228 using a 5 generation relationship matrix with unknown ancestors assigned to genetic
229 groups as defined by the breed types used to estimate heterosis and recombination
230 co-efficients. The mixed linear model can be written as

231

$$232 \quad y = Xb + ZQg + Zu + e$$

233

234 where **y** is the vector of observations, **b** is the vector of fixed effects, **g** is the vector
235 of genetic groups, **u** is the vector of random effects, **e** is the vector of residual effects
236 and the **X**, **Z** and **Q** matrices are the respective incidence matrices. The fixed effects
237 included in the model to estimate genetic parameters were those found to be
238 significant as described earlier. To estimate genetic and residual co-variances
239 between the traits a series of bi-variate models were undertaken using ASReml. For
240 the primal cut yield traits; Topside, Silverside, Knuckle, Rump, Striploin and Fillet a
241 separate set of analyses were undertaken using the same methodology but also after
242 adjusting for carcass weight.

243

244 **Results**

245

246 *Phenotypic data*

247 A summary of the phenotypic data is contained in table 1. Animals were slaughtered
248 on average at 627 days (20.5 months) of age with an average carcass weight of 354
249 kg. In total the six VIA primal cut yields sum to 104.72 kg and account for 29.6% of
250 the total carcass weight. The coefficients of variation for all primal cut yields and

251 carcass weight ranged from 0.16 to 0.19. Coefficients of variation for slaughter age,
252 conformation class and fat score were higher ranging from 0.25 to 0.27. Average
253 conformation and fat values were 24.75 and 24.19 respectively, corresponding to a
254 value of R (good muscle development) for EUROP conformation class and to a value
255 of three (average fat cover over the carcass with slight deposits of fat in the thoracic
256 cavity) in the EUROP fat class.

257

258 *Heritability*

259 All carcass traits were moderately heritable with heritability estimates ranging from
260 0.32 for EUROP fat to 0.46 for the Topside primal yield (Table 2). Whilst the
261 heritability estimates were similar for all primal cut yields, there were differences in
262 the variances. The primal cut yield for Fillet has the lowest phenotypic variation at
263 0.43; it was also seen in Table 1 to be the smallest primal cut of those considered in
264 this study. Both Topside and Silverside primal cuts were observed to be the larger
265 primal cuts in the study and also showed the higher phenotypic variances. However,
266 the genetic coefficient of variation for all six primal yields was approximately 0.13.
267 Carcass weight and EUROP conformation and fat class all had higher phenotypic
268 variances estimates and had genetic coefficient of variation of 0.06, 0.11 and 0.15,
269 respectively. When primal cut yields were also adjusted for carcass weight the
270 heritability estimates were lower, but still moderate, ranging from 0.23 for Fillet to
271 0.29 for Knuckle primal cut yield. Phenotypic variances were also reduced.

272

273 *Genetic and phenotypic correlations*

274 Strong positive genetic correlations between carcass weight and all the primal cut
275 yields were estimated when traits were age adjusted (Table 3). These correlations

276 were much reduced and only low to moderate in size when the primal cut yields were
277 also adjusted for carcass weight (Table 4). Strong positive phenotypic correlations
278 between these traits were also estimated, but once primal cut yields were adjusted
279 for carcass weight, phenotypic correlations were not significantly different from zero.
280

281 All six primal cut yields had strong positive - almost unity - genetic correlations to
282 each other when adjusted for slaughter age. When the primal cut yields were also
283 adjusted for carcass weight, the strength of the correlations reduced, but was still
284 strong and positive; genetic correlations ranged from 0.40 between Fillet and
285 Striploin to 0.92 between Topside and Silverside. This same trend can be observed
286 with estimates of the phenotypic correlations; when the primal cut yields were
287 adjusted for slaughter age and carcass weight phenotypic correlations ranged from
288 0.22 between Fillet and Striploin to 0.80 between Topside and Silverside.
289

290 EUROP conformation was estimated to have a moderate positive genetic correlation
291 with carcass weight, and strong positive genetic correlations with the primal cut yields
292 (regardless of whether carcass weight was adjusted for). A moderate negative
293 genetic correlation was estimated with EUROP fat. In all cases, EUROP fat was
294 estimated to have low to moderate negative genetic correlations with carcass weight
295 and the primal cut yields. Generally the size of the genetic correlations with primal cut
296 yields increased when they were adjusted for carcass weight. Moderate positive
297 phenotypic trends were estimated between EUROP conformation, and carcass
298 weight and primal cut yields (regardless of whether primal cut yields were adjusted
299 for carcass weight). Generally, the phenotypic correlations between EUROP fat and
300 the other traits were not significantly different from zero or were low and negative.

301 After adjusting for carcass weight, the phenotypic correlations between EUROP fat
302 and the primal cut yields were low and negative. All correlation estimates show that
303 animals that have genetically heavier carcasses will also have increased primal cut
304 yields, increased muscling of the carcass and decreased subcutaneous fat.

305

306 **Discussion**

307 The objective of this study was to estimate genetic parameters for abattoir VIA primal
308 cut yields of UK commercial cross bred animals and determine if the traits are
309 suitable for genetic evaluation. This was the first study in the UK estimating genetic
310 parameters from large numbers of commercial cattle with VIA carcass traits recorded.
311 Outside of the UK, there has only been a small number of studies estimating genetic
312 parameters for individual carcass cut yield (Cantet *et al.*, 2003; Pabiou *et al.*, 2009)
313 or with traits predicted from digital imaging (Pabiou *et al.*, 2011a). With 17,765
314 carcass records, this study is one of the largest studies to consider primal cut yields
315 with most studies having less than 1,000 animals (Cantet *et al.*, 2003, Pabiou *et al.*,
316 2009; 2011b) and only one other sizable data set with Pabiou *et al.* (2011a)
317 analysing 52,722 carcasses.

318

319 The UK beef industry consists of many different breeds with 94% of the prime
320 slaughter population being cross bred and through cross breeding, dairy genetics
321 contributes 28% of the genes in the prime slaughter population (Todd *et al.*, 2011).
322 The dataset used in this study was reflective of the prime slaughter population
323 described by Todd *et al.* (2011). In the edited dataset the average carcass weight of
324 354kg was similar to the 2013 national average of 341kg reported by EBLEX (2014).

325

326 Heritability estimates were reported in Table 2. The six primal cut yields were
327 estimated to have moderate heritabilities in both models considered in this study.
328 Adjusting for carcass weight reduced the heritability and phenotypic variance
329 estimates of primal cut yields. However the primal cut yields were adjusted for
330 carcass weight to avoid encouraging the industry to select for larger animals, instead
331 setting a breeding objective of increasing the proportion of weight in valuable primal
332 cut yields for a given carcass weight means more valuable carcasses and not just
333 bigger carcasses. Estimates in this study were comparable to those reported in the
334 literature. Pabiou *et al.* 2009 considered carcass dissection data from an
335 experimental (n=413) and a commercial (n=635) data set similar to the UK data set
336 used in this study. The Primal cut yields were adjusted for age and heritability
337 estimates in the experimental data set ranged from 0.14 (0.16) for Rib roast to 0.86
338 (0.23) for the Round primal cut. Similarly, in the commercial data set heritability of
339 hind quarter cuts ranged from 0.40 (0.19) for Rib roast to 0.63 (0.20) for Fillet. In a
340 much larger commercial data set, Pabiou *et al.* (2011a) estimated heritabilities
341 ranging from 0.17 (0.018) for very high value cuts (Rib roast, Striploin and Fillet) to
342 0.40 (0.024) for high value cuts (Sirloin and the round) predicted from VIA. This same
343 study considered the traits separately for heifers and steers and heritability estimates
344 were generally higher for heifers and showed strong positive genetic correlations
345 between the sexes (correlations ranged from 0.54 (0.14) to 0.76 (0.07)).

346

347 There have been more studies reported for carcass weight and EUROP conformation
348 and fat. The moderate heritability estimated for carcass weight is similar to the
349 average estimate of 0.40 reported by Rios Utrera and Van Vleck (2004) from a
350 review of 56 studies. Hickey *et al.* (2007) reported carcass weight heritability

351 estimates from a number of different breeds in the Irish population ranging from 0.17
352 in Angus and Belgian Blue cattle to 0.65 in Charolais cattle. In a Finland study
353 considering 5 beef cattle breeds, carcass weight heritability estimates ranged from
354 0.39 to 0.48 (Kause *et al.*, 2015). A moderate heritability was estimated for both
355 EUROP conformation and fat class and these estimates are similar to those reported
356 by Pabiou *et al.* (2011a). In a Swedish population, Eriksson *et al.* (2003) estimated
357 heritability for conformation of 0.22 in Hereford and 0.34 in Charolais. In the same
358 study heritability estimates for carcass fat were 0.38 and 0.27 for Charolais and
359 Hereford, respectively. In Finland, Kause *et al.* (2015) estimated heritabilities of
360 between 0.30 to 0.44 for conformation and 0.29 to 0.44 for fat. The study by Hickey
361 *et al.* (2007) showed a wide variation in carcass conformation and fat heritability
362 estimates across the breeds considered. For carcass conformation, heritabilities
363 ranged from 0.04 for Friesian to 0.36 for Limousin. For carcass fat, heritability
364 estimates ranged from 0.00 for Limousin to 0.40 for Simmental.

365

366 This study found that there were moderate to strong genetic correlations between the
367 carcass traits analysed (Table 3 and 4). Carcass weight was found to be strongly
368 positively correlated with carcass conformation (0.53) and negatively correlated with
369 carcass fat (-0.14). Conformation and fat were also had a moderately negative
370 correlation (-0.27). Pabiou *et al.* (2011a) also found these genetic relationships in
371 steers, although with a lower genetic correlation between carcass weight and
372 conformation (0.35). Hickey *et al.* (2007) found positive genetic correlations between
373 carcass weight and conformation (0.11) but, in contrast to our findings, estimated
374 positive genetic correlation between carcass weight and fat (0.26), and between
375 conformation and fat (0.44). Kause *et al.* (2015) also estimated positive correlations

376 between carcass weight and fat with genetic correlation estimates ranging from 0.08
377 to 0.28. In agreement with our results, other studies also found positive genetic
378 correlations between conformation and carcass weight, with values ranging from 0.25
379 to 0.66 (Van der Werf *et al.*, 1989; Hirooka *et al.*, 1996; Liinamo *et al.*, 1999;
380 Parkkonen *et al.*, 2000; Kause *et al.*, 2015) in dairy and dual purpose cattle herds.

381
382 Very strong, almost unity, genetic correlations (0.92+) were estimated between the
383 VIA primal cut yields. Adjusting for carcass weight reduced the correlations with
384 estimates ranging from 0.40 between Fillet and Striploin to 0.92 between Topside
385 and Silverside. These strong positive correlations suggests that selection pressure
386 for a given primal cut will result in increased yields for all six primal cuts, but as
387 carcass weight has been adjusted for in the model, selection will not indirectly select
388 for heavier carcass weights. High positive genetic correlations were also estimated
389 by Pabiou *et al.* (2009) from dissection carcass data with estimates ranging from 0.67
390 between Fillet and Striploin and 0.93 between Fillet and Round. Using predicted
391 yields Pabiou *et al.* (2011a) estimated genetic correlations ranging from 0.45
392 between low value cuts and medium value cuts to 0.89 between high value cuts and
393 very high value cuts.

394

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401

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453 **Table 1** Overall mean, standard deviation, minimum, maximum and coefficient of
 454 variation for Visual Image Analysis (VIA) carcass traits from 17,765 cross bred prime
 455 slaughter commercial cattle

Trait ¹	N	Mean	SD	Min	Max	CV
Slaughter age (days)	17765	627.0	157.81	365.0	1095.0	0.25
Carcass Weight (kg)	17765	353.91	55.04	189.10	550.20	0.16
Topside (kg)	17765	23.64	4.01	12.96	37.74	0.17
Silverside (kg)	17765	28.50	5.37	14.86	46.26	0.19
Knuckle (kg)	17765	14.61	2.51	6.80	23.70	0.17
Rump (kg)	17765	15.08	2.65	6.90	23.54	0.18
Striploin (kg)	17765	16.44	2.90	8.02	26.18	0.18
Fillet (kg)	17765	6.46	1.14	3.46	10.92	0.18
Conformation (1-42 scale)	17765	24.75	6.79	3.00	42.00	0.27
Fat (1-42 scale)	17765	24.19	6.46	3.00	42.00	0.27

456 N = Number of animals; Mean = Mean of the trait; SD = Standard deviation of trait; Min = Minimum
 457 trait value; Max = Maximum trait value; CV = coefficient of variation

458 ¹ Slaughter age is the age of the animal at slaughter; Carcass weight is the weight of the carcass at
 459 slaughter; Topside, Silverside, Knuckle, Rump, Striploin and Fillet are all primal cut yields from the
 460 total carcass predicted using VIA; Conformation and Fat is the EUROP conformation and fat classes,
 461 predicted using VIA and converted to a numerical 1-42 scale; higher values represent more muscular
 462 carcasses for conformation and higher levels of fat for fat

463

464 **Table 2** Genetic, residual and phenotypic variances and trait heritability (standard
 465 errors parenthesis) estimates for Visual Image Analysis (VIA) carcass traits from
 466 17,765 cross bred prime slaughter commercial cattle

Trait ¹	σ_a^2	σ_e^2	σ_p^2	h^2
Age adjusted				
Carcass Weight	368.20 (28.96)	481.45 (23.44)	849.66 (11.21)	0.43 (0.03)
Topside	2.31 (0.18)	2.77 (0.14)	5.07 (0.07)	0.46 (0.03)
Silverside	3.63 (0.28)	4.58 (0.23)	8.22 (0.11)	0.44 (0.03)
Knuckle	0.86 (0.07)	1.07 (0.05)	1.93 (0.03)	0.45 (0.03)
Rump	0.91 (0.07)	1.22 (0.06)	2.13 (0.03)	0.43 (0.03)
Striploin	0.92 (0.08)	1.36 (0.06)	2.28 (0.03)	0.40 (0.03)
Fillet	0.18 (0.01)	0.25 (0.01)	0.43 (0.01)	0.42 (0.03)
Conformation	5.53 (0.45)	7.30 (0.36)	12.83 (0.17)	0.43 (0.03)
Fat	6.36 (0.61)	13.58 (0.51)	19.94 (0.25)	0.32 (0.03)
Weight adjusted				
Topside	0.25 (0.03)	0.77 (0.02)	1.02 (0.01)	0.25 (0.03)
Silverside	0.38 (0.04)	1.03 (0.04)	1.42 (0.02)	0.27 (0.03)
Knuckle	0.15 (0.02)	0.37 (0.01)	0.53 (0.01)	0.29 (0.03)
Rump	0.15 (0.02)	0.41 (0.01)	0.57 (0.01)	0.27 (0.03)
Striploin	0.10 (0.01)	0.26 (0.01)	0.37 (0.01)	0.28 (0.03)
Fillet	0.02 (0.003)	0.07 (0.002)	0.09 (0.001)	0.23 (0.03)

467 σ_a^2 = Genetic variance component; σ_e^2 = Residual variance component; σ_p^2 = Phenotypic variance
 468 component; h^2 = heritability

469 ¹ Carcass weight is the weight (kg) of the carcass at slaughter; Topside, Silverside, Knuckle, Rump,
 470 Striploin and Fillet are all primal cut yields(kg) predicted from the total carcass using VIA;
 471 Conformation and Fat is the EUROP conformation and fat classes, predicted using VIA and converted
 472 to a numerical 1-42 scale; higher values represent more muscular carcasses for conformation and
 473 higher levels of fat for fat

474 **Table 3** Genetic (above diagonal) and phenotypic (below diagonal) correlations estimates (standard errors in parenthesis) for age
 475 adjusted Visual Image Analysis (VIA) primal cut yield carcass traits from 17,765 cross bred prime slaughter commercial cattle

Trait ¹	CWT	TOP	SIL	KNU	RUM	STR	FIL	CON	FAT
CWT		0.95 (0.01)	0.94 (0.01)	0.91 (0.01)	0.91 (0.01)	0.94 (0.01)	0.94 (0.01)	0.53 (0.04)	-0.14 (0.06)
TOP	0.89 (0.002)		0.99 (0.002)	0.98 (0.003)	0.95 (0.01)	0.95 (0.01)	0.98 (0.003)	0.70 (0.03)	-0.26 (0.06)
SIL	0.91 (0.002)	0.96 (0.001)		0.97 (0.004)	0.95 (0.01)	0.95 (0.01)	0.98 (0.003)	0.72 (0.03)	-0.27 (0.06)
KNU	0.85 (0.003)	0.95 (0.001)	0.92 (0.001)		0.96 (0.01)	0.94 (0.01)	0.96 (0.01)	0.73 (0.03)	-0.26 (0.06)
RUM	0.86 (0.002)	0.89 (0.01)	0.87 (0.002)	0.89 (0.002)		0.95 (0.01)	0.94 (0.01)	0.73 (0.03)	-0.21 (0.06)
STR	0.92 (0.002)	0.89 (0.002)	0.89 (0.002)	0.87 (0.002)	0.88 (0.002)		0.93 (0.01)	0.73 (0.03)	-0.16 (0.06)
FIL	0.88 (0.002)	0.95 (0.001)	0.95 (0.001)	0.90 (0.002)	0.84 (0.003)	0.85 (0.003)		0.65 (0.03)	-0.29 (0.06)
CON	0.44 (0.01)	0.56 (0.01)	0.60 (0.01)	0.57 (0.01)	0.60 (0.01)	0.58 (0.01)	0.51 (0.01)		-0.27 (0.05)
FAT	0.17 (0.01)	0.02 (0.01)	0.03 (0.01)	0.02 (0.01)	0.08 (0.01)	0.14 (0.01)	0.03 (0.01)	0.00 (0.01)	

476 CWT = Carcass weight; TOP = Topside; SIL = Silverside; KNU = Knuckle; RUM = Rump; STR = Striploin; FIL = Fillet; Conformation = Conformation; Fat =
 477 Fat

478 ¹ Carcass weight is the weight (kg) of the carcass at slaughter; Topside, Silverside, Knuckle, Rump, Striploin and Fillet are all primal cut yields(kg) predicted
 479 from the total carcass using VIA; Conformation and Fat is the EUROP conformation and fat classes, predicted using VIA and converted to a numerical 1-42
 480 scale; higher values represent more muscular carcasses for conformation and higher levels of fat for fat

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483 **Table 4** Genetic (above diagonal) and phenotypic (below diagonal) correlations estimates (standard errors in parenthesis) for
 484 weight adjusted Visual Image Analysis (VIA) primal cut yield carcass traits from 17,765 cross bred prime slaughter commercial
 485 cattle

Trait ¹	CWT	TOP	SIL	KNU	RUM	STR	FIL	CON	FAT
CWT		0.17 (0.06)	0.25 (0.06)	0.28 (0.06)	0.23 (0.06)	0.11 (0.06)	0.22 (0.06)	0.53 (0.04)	-0.14 (0.06)
TOP	-0.09 (0.01)		0.92 (0.02)	0.87 (0.02)	0.69 (0.04)	0.56 (0.05)	0.84 (0.03)	0.78 (0.03)	-0.43 (0.06)
SIL	0.02 (0.01)	0.80 (0.003)		0.85 (0.02)	0.69 (0.04)	0.57 (0.05)	0.82 (0.02)	0.84 (0.02)	-0.44 (0.06)
KNU	0.03 (0.01)	0.78 (0.003)	0.67 (0.01)		0.75 (0.03)	0.60 (0.04)	0.73 (0.04)	0.79 (0.03)	-0.35 (0.06)
RUM	0.02 (0.01)	0.53 (0.01)	0.43 (0.01)	0.58 (0.005)		0.65 (0.04)	0.60 (0.05)	0.77 (0.03)	-0.21 (0.06)
STR	0.01 (0.01)	0.42 (0.01)	0.37 (0.01)	0.40 (0.01)	0.47 (0.01)		0.40 (0.06)	0.81 (0.03)	-0.11 (0.06)
FIL	0.04 (0.01)	0.74 (0.003)	0.75 (0.003)	0.59 (0.01)	0.36 (0.01)	0.22 (0.01)		0.59 (0.04)	-0.46 (0.06)
CON	0.44 (0.01)	0.45 (0.01)	0.56 (0.01)	0.44 (0.01)	0.51 (0.01)	0.53 (0.01)	0.31 (0.01)		-0.27 (0.05)
FAT	0.17 (0.01)	-0.30 (0.01)	-0.30 (0.01)	-0.25 (0.01)	-0.13 (0.01)	-0.03 (0.01)	-0.26 (0.01)	0.00 (0.01)	

486 CWT = Carcass weight; TOP = Topside; SIL = Silverside; KNU = Knuckle; RUM = Rump; STR = Striploin; FIL = Fillet; Conformation = Conformation; Fat =
 487 Fat

488 ¹ Carcass weight is the weight (kg) of the carcass at slaughter; Topside, Silverside, Knuckle, Rump, Striploin and Fillet are all primal cut yields(kg) predicted
 489 from the total carcass using VIA; Conformation and Fat is the EUROP conformation and fat classes, predicted using VIA and converted to a numerical 1-42
 490 scale; higher values represent more muscular carcasses for conformation and higher levels of fat for fat

